



Blast 2 Sequences results

PubMed

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BLAST

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Taxonomy

Structure

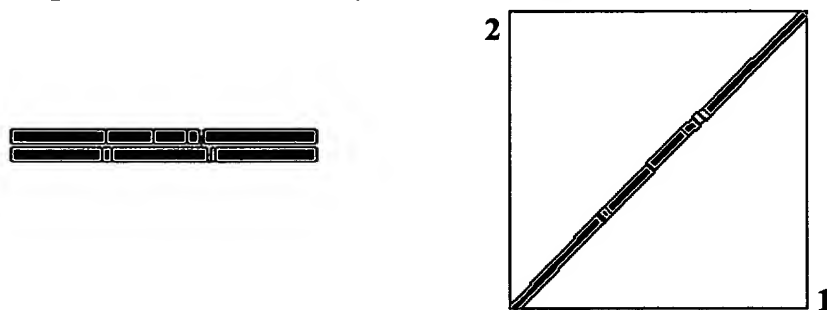


BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ **Align**

Sequence 1 **lcl|seq_1** Length 862 (1 .. 862)

Sequence 2 **lcl|seq_2** Length 859 (1 .. 859)



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NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1202 bits (3110), Expect = 0.0

Identities = 637/869 (73%), Positives = 704/869 (80%), Gaps = 17/869 (1%)



Query: 1 MERAESSSTEPAKAIKPIDRKSVHQICSGQVVLSTAVKELVENS LDAGATNIDLKLKD 60
 ME+ E STE AKAIKPID KSVHQICSGQV+LSLSTAVKEL+ENS+DAGAT IDL+LKD
 Sbjct: 1 MEQTGEGVSTECAKAIKPIDGKSVHQICSGQVILSLSTAVKELIENSVDAGATTIDRLRKD 60

Query: 61 YGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120
 YGVDLIEVSDNGCGVEEENFEGL LKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV
 Sbjct: 61 YGVDLIEVSDNGCGVEEENFEGLALKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120

Query: 121 TISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQORNIKE 180
 TISTCH SA VGTRL+FDHNGKI QKTPYPRP+GTTVSVQ LF TLPVR+KEFQORNIKE
 Sbjct: 121 TISTCHGSASVGTRLVFDHNGKITQKTPYPRPKGTTVSVQHLYFTLPVRYKEFQORNIKE 180

Query: 181 YAKMVQVLHAYCIIISAGIRVSCNTQLGQGKRQPVVCTGGSPSIKENIGSVFGQKQLQSLI 240
 Y+KMOVVL AYCIISAG+RVSCNTQLGQGKR VVCT G+ +KENIGSVFGQKQLQSLI
 Sbjct: 181 YSKMVQVLQAYCIIISAGVRVSCNTQLGQGKRHAVVCTSGTSGMKENIGSVFGQKQLQSLI 240

Query: 241 PFVQLPPSDSVCEEYGLSCSDALHNLFF--YISGFISQCTHGVGRSSTDROFFFINRRPCD 298
 PFVQLPPSD+VCEEYGLS S H F + + F S T G T F R P
 Sbjct: 241 PFVQLPPSDAVCEEYGLSTSGR-HKTFTSTFRASFHSARTAPGGVQQTG-SFSSSIRGPVT 298

Query: 299 PAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTDPKRQILLQEEKLLLAVLKTS 358
 + L YHMYNRHQYPFVVLN+SVSECVDINVTDPKRQILLQEEKLLLAVLKTS
 Sbjct: 299 QQRSLSLSMRFYHMYNRHQYPFVVLNVSDSECVDINVTDPKRQILLQEEKLLLAVLKTS 358

Query: 359 LIGMFDSDVNKLNVSQQLLDVEGNLIKMAADLEKPMVEKQDQSPSLR-TGEEKKDVSI 417
 LIGMFDSD NKLNV+QQQLLDVEGNL+K+H A+LEKP+ KQD SPSL+ T +EK+ SI

Sbjct: 359 LIGMFDSDANKLNVNQQLLDVEGNLVKLHTAELEKPVPGKQDNPSLSTADEKRVASI 418

Query: 418 SRLREAFSLRHTTENKPHSPKTPPEPRRSPLGQKRGMLSSSTSGAISDKGVLRPQKEAVSS 477
 SRLREAFSL T E K P+T E RS +KRG+LSS S IS +G+ Q + VS

Sbjct: 419 SRLREAFSLHPTKEIKSRGPETAELTRSFPSSEKRGVLSSYPSDVISYRGLRGSQDKLVSP 478

Query: 478 SHGPSDPTDRAEVEKDSGHGSTSVDSSEG-FSIPDTGSHCSSEYAASSPGDRGSQEHVDSQ 536
 + P D DR ++EKDSG STS SE FS P+ S SS+Y SS DR SQE ++

Sbjct: 479 TDSPGDCMDREKIEKDSGLSSTSAGSEEEFSTPEVASSFSSDYNVSSLEDPRSQETINCG 538

Query: 537 E---KAPETDDSFSDVDCHSNQEDTGCKFRVLPQPTNLATPNTKRFKKEEILSSSDICQK 593
 + + P T S ED G + + LP L+ N KRFK EE S+ +I Q+

Sbjct: 539 DLDCRPPGTGQSLKP-----EDHGYQCKALPL-ARLSPTNAKRFKTEERPSNVNISQR 590

Query: 594 LVNTQDMSASQVDVAVKINKKVPLDFSMSSLAKRIKQLHHEAQQSEGEQNYRKFRAKIC 653
 L Q SA++VDVA+K+NK++V L+FS+SSLAKR+KQL H Q++ E +YRKFRAKIC

Sbjct: 591 LPGPQSTSAAEVDVAIKMNKRIVLLEFSLSSLAKRMKQLQHLKAQNKHEL SYRKFRAKIC 650

Query: 654 PGENQAAEDELRLKEISKTMFAEMEIIQGFNLGFIITKLNEDIFIVDQHATDEKYNFEMLO 713
 PGENQAAEDELRLKEISK+MFAEMEII+QGFNLGFI+TKL ED+F+VDQHA DEKYNFEMLO

Sbjct: 651 PGENQAAEDELRLKEISKSMFAEMEILGQFNLGFIIVTKLKEDLFLVDQHADEKYNFEMLO 710

Query: 714 QHTVLQGGQRLIAPQTLNLTAVNEAVLIENLEIFRKNNGFDFVIDENAPVTERAKLISLPTS 773
 QHTVLQ QRLI PQTNLNLTAVNEAVLIENLEIFRKNNGFDFVIDE+APVTERAKLISLPTS

Sbjct: 711 QHTVLQAQRLITPQTLNLTAVNEAVLIENLEIFRKNNGFDFVIDEDAPVTERAKLISLPTS 770

Query: 774 KNWTFGPQDVDELIFMLSDSPGVMCRPSRVQMFASTRACRKSVMIGTALNTSEMKKLITH 833
 KNWTFGPQD+DELIFMLSDSPGVMCRPSRV+QMFASTRACRKSVMIGTALN SEMKKLITH

Sbjct: 771 KNWTFGPQDIDELIFMLSDSPGVMCRPSRVQMFASTRACRKSVMIGTALNASEMKKLITH 830

Query: 834 MGEMDHPWNCPHGRPTMRHIANLGVISQN 862
 MGEMDHPWNCPHGRPTMRH+ANL VISQN

Sbjct: 831 MGEMDHPWNCPHGRPTMRHVANLDVISQN 859

CPU time: 0.17 user secs. 0.04 sys. secs 0.21 total secs.

Lambda K H
 0.315 0.131 0.371

Gapped
 Lambda K H
 0.267 0.0410 0.140

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Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 6158

Number of Sequences: 0

Number of extensions: 502

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 859

length of database: 461,760,005

effective HSP length: 136

effective length of query: 723

effective length of database: 461,759,869

effective search space: 333852385287
effective search space used: 333852385287
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 79 (35.0 bits)

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